

PubMed

Entrez

BLAST

OMIMO

Taxonomy

Structure

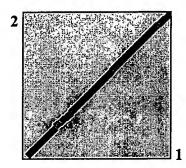
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix BLOSUM62 gap open: 11 gap extension: 1	
x_dropoff: 50 expect: 10.0000 wordsize: 3 Filter View option Standard	
Masking character option X for protein, n for nucleotide Masking color option Black	
Show CDS translation Align	

Sequence 1: lcl|Navarro Length = 569 (1 .. 569)

Sequence 2: lcl|WatsonLength = 566 (1 .. 566)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



883 bits (2281), Expect = 0.0Identities = 454/559 (81%), Positives = 475/559 (84%), Gaps = 21/559 (3%) 83 PTCVLSQVQLKESGPGLVKPSQTLSLTCTVSGLSLSSNSVGWVRQAPGKGLEWVGFRSGG Query SQVQLKESGPGLVKPSQTLSLTCTVSG SL+S +VGWV + PTCAPSQVQLKESGPGLVKPSQTLSLTCTVSGFSLTSYTVGWVARLQEKDWNMLRLYVIV Sbjct 16 EEEYYNPALKSRATITEDAAKSQVYLDAEQVTGEATAVYYCAEV -YNNYLYYGI 136 Query 84 LKSRA+IT DA+KSQVYL +T E TAVYYCA GVQTSTQTLKSRAS ITRDASKSQVYLTLNSLTVEDTAVYYCARSLPVSGNGYSLVNYWGQ 135 Sbjct 76 137 KELGARGLLVTVSSVSKQAPLIFPLAACCKDTKTTNITLGCLVKGYFPG----AWDAGPL Query VTVSSVSKQ+P+I PLAACCKDTKTTNITLGCLVKGYFP -----VTVSSVSKQSPIILPLAACCKDTKTTNITLGCLVKGYFPEPVTVTWDAGSL Sbjct 136 188 NPSTMTFPAVFDQTSGLYTTISRVVASGKWAKQKFTCGVVHSQETFNKTFNACIVTFTPP 193 Query N ST+TFPAVFDQTSGLYTTISRVVASGKWAKQKFTC VVHSQETFNKTFNACIVTFTPP Sbjct NRSTITFPAVFDQTSGLYTTISRVVASGKWAKQKFTCNVVHSQETFNKTFNACIVTFTPP 248

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Query 253 TVKLFHSSCDPGGDSHTTIQLLCLISDYTPGDIDIVWLIEGQKVDEQFPTQASMKQEGSW 312
            TVKLFHSSCDPGGDSHTTIQLLCLISDYTPGDIDIVWLI+GQKVDEQFP
      249 TVKLFHSSCDPGGDSHTTIQLLCLISDYTPGDIDIVWLIDGQKVDEQFPQHGLVKQEGKL
Sbjct
      313 PPTHSELNINGGQWASENTYTCQVTYK--DMIFNQARKCTESDPPGVSVYLSPPSPLDLY
                                                                          370
Ouery
              THSELNI QGQWASENTYTCQVTYK D++ + RKCTES+P GVSVYLSPPSPLDLY
       309 ASTHSELNITQGQWASENTYTCQVTYKRHDLLRTRPRKCTESEPRGVSVYLSPPSPLDLY
Sbjct
      371 VSKTPKITCLVVDLANVQGLSLNWSRESGEPLQKHTLATSEQFNKTFSVTSTLPVDTTDW
                                                                          430
Query
            VSK+PKITCLVVDLANVQGLSLNWSRESGEPLQKHTLATSEQFNKTFSVTSTLPVDTTDW
      369 VSKSPKITCLVVDLANVQGLSLNWSRESGEPLQKHTLATSEQFNKTFSVTSTLPVDTTDW
                                                                         428
Sbjct
      431 IEGETYKCTVSHPDLPREVVRSIAKAPGKRLSPEVYVFLPPEEDQSSKDKVTLTCLIQNF
Query
            IEGETYKCTVSHPDLPREVVRSIAKAPGKRLSPEVYVFLPPEEDQSSKDKVTLTCLIQNF
Sbjct 429 IEGETYKCTVSHPDLPREVVRSIAKAPGKRLSPEVYVFLPPEEDQSSKDKVTLTCLIQNF
                                                                          488
Query 491 FPADISVQWRRNNVLIQTDQQATTRPQKANGPDPAFFVFSRLEVSRAEWEQKNKFACKVV
            FPADISVQW RNNVLIQTDQQATTRP K+ P PAFFVFSRLEVSRAEWEQKNKFACKVV
      489 FPADISVQWLRNNVLIQTDQQATTRP-KSQWPRPAFFVFSRLEVSRAEWEQKNKFACKVV 547
Sbjct
       551 HEALSORTLOKEVSKDPGK 569
Query
            HEALSORTLOKEVSKDPGK
Sbjct 548 HEALSQRTLQKEVSKDPGK 566
                                                           0.05 total secs.
                                  0.01 sys. secs
            0.04 user secs.
CPU time:
Lambda
           K
                 Η
   0.315
           0.131
                     0.398
Gapped
Lambda
           K
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 2833
Number of extensions: 1496
Number of successful extensions: 20
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 569
Length of database: 1,125,694,017
Length adjustment: 138
Effective length of query: 431
Effective length of database: 1,125,693,879
Effective search space: 485174061849
Effective search space used: 485174061849
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.6 bits)
S2: 81 (35.8 bits)
```